

Camille Scott

Permanent Address

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(as of May 2023)

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| EDUCATION | University of California Davis , Davis, CA <i>PhD., Computer Science, Lab for Data Intensive Biology</i> <i>Dissertation: Streaming Methods for Assembly Graph Analysis</i> | 2015-2022 |
| | Michigan State University , East Lansing, MI <i>GED Lab, PhD. student, Computer Science</i> | 2012-2015 |
| | Alma College , Alma, MI <i>B.S., Computer Science</i> | 2008-2012 |
| WORK | Systems Administrator at UC Davis HPCCF <i>Provide scientific computing support to the College of Biological Sciences for the High Performance Computing Core Facility. Co-lead design and deployment of the Franklin cluster consisting of 11 compute and GPU nodes with 2PB of attached network storage: designed and maintain reproducible software stack for genomics and cryo-EM workflows using Spack and Conda; design and maintenance of core software and libraries for scheduling and infrastructure; co-designed and implemented complete refactoring of Puppet configuration codebase for automated configuration management; communicate and implement stakeholder and user needs; collaborate with researchers on deployment, optimization, and use of their scientific software in the HPC environment; deploy and maintain user documentation and tutorials.</i> | 7/2022-present |
| | Genomic Data Specialist at APHL <i>Processed SARS-CoV-2 genomes through contract work mediated by the Association of Public Health Labs in the COVID-19 pandemic effort. Quality controlled genome assemblies, managed genome metadata, wrote processing workflows, and submitted genomes to GISAID for public archiving.</i> | 5/2021-8/2022 |
| | Teaching Assistant at UC Davis <i>ECS132: Probabilistic and Statistical Modeling in Computer Science. Graded assignments and exams, held office hours, gave one-on-one student help, and developed course materials.</i> | Spring 2021 |
| | Teaching Assistant at UC Davis <i>GGG201B: Genomics. Provided student help and graded take-home assignments.</i> | Winter 2021 |

Junior Specialist at **UC Davis**

6/2015-10/2015

Scientific software development for the khmer project; worked on core functionality (high performance C++ with CPython bindings, Python CLI), automated testing, continuous integration, packaging and distribution.

Workshop Teaching Assistant at **Marine Biological Laboratory**

8/2013

TA for the two-week intensive Strategies and Techniques for Analyzing Microbial Population Structures. Assisted students with hands-on bioinformatics training, developed materials, and taught portions.

Lead Instructor at **Michigan State University**

Fall 2012

CSE101: Primary instructional interface for three sections of 30 undergraduates each; delivered lecture, graded assignments and exams, held office hours and study sessions.

Teaching Assistant (TA) at **Alma College**

2011-2012

Intro to Computer Science. Assisted students during programming laboratory sessions.

MANUSCRIPTS

Scott, C., & Brown, C. T. (2022). *Streaming Construction of the Compact de Bruijn Graph*. In prep.

Reiter, T., Brooks, P. T., Irber, L., Joslin, S. E., Reid, C. M., Scott, C., ... & Pierce, N. T. (2020). *Streamlining Data-Intensive Biology With Workflow Systems*. BioRxiv.

Neches, R. Y., & Scott, C. (2018). *SuchTree: Fast, thread-safe computations with phylogenetic trees*. Journal of Open Source Software, 3(26), 678.

Scott, C. (2017). *shmlast: An improved implementation of Conditional Reciprocal Best Hits with LAST and Python*. The Journal of Open Source Software, 2017.

Ren, J., Chung-Davidson, Y. W., Yeh, C. Y., Scott, C., Brown, T., & Li, W. (2015). *Genome-wide analysis of the ATP-binding cassette (ABC) transporter gene family in sea lamprey and Japanese lamprey*. BMC genomics, 16(1), 436.

Crusoe, M. R. et. al. (2015). *The khmer software package: enabling efficient nucleotide sequence analysis*. F1000Research, 4.

Aleksic, J., Alexa, A., Attwood, T. K., Hong, N. C., Dahlö, M., Davey, R., ..., & Lahti, L. (2014) *The open science peer review oath*. F1000Research, 3.

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| HONORS AND AWARDS | USDA / MSU / National Needs Fellow | 2013-2015 |
| | Binghamton University / Research Experience for Undergrads | 2011 |
| | Alma College / Distinguished Scholar Award | 2008-2012 |
| PROFESSIONAL ACTIVITIES | Lead Instructor for workshop at UC Davis , <i>ANGUS: Next-Gen Sequence Analysis Workshop</i> | Summer 2017 |
| | Participant in Workshop at University of California Davis , <i>Software Carpentry "Train the Trainers"</i> | 01/2015 |
| | Participant in Workshop at The Genome Analysis Center (TGAC) , <i>AllBio Open Science & Reproducibility Best Practices Workshop</i> | 09/2014 |
| | TA for SROP Workshop at Michigan State University , <i>Statistics Bootcamp with the Summer Research Opportunities Program</i> | 05/2014 |
| | Presenter at Michigan State University , <i>Summer Research Opportunities (SROP) Workshop</i> | 5/2013 |
| | Workshop TA at California Institute of Technology , <i>Workshop on Microbial Bioinformatics</i> | 10/2013 |
| | <i>Co-founder, Alma College Association for Computing Machinery</i> | 2012 |
| SOFTWARE | Author and maintainer of cheeto , <i>Python library and CLI tools for HPC management</i> github.com/ucdavis/cheeto | |
| | Author and maintainer of goetia , <i>C++ and Python library and command line tools for streaming sequence analysis</i> github.com/camillescott/goetia | |
| | Author and maintainer of debruijnal-enhance-o-tron , <i>pytest fixtures for random de Bruijn graph generation</i> github.com/camillescott/debruijnal-enhance-o-tron | |
| | Author and maintainer of dammit , <i>a tool for easy de novo transcriptome annotation</i> github.com/camillescott/dammit | |
| | Author and maintainer of shmlast , <i>an implementation of conditional reciprocal best hits with Python and LAST</i> github.com/camillescott/shmlast | |
| | Contributor to khmer Protocols Project , | |

Protocols for cloud-based de novo RNA-seq and metagenomic analyses
khmer-protocols.readthedocs.org

Contributor to open source **khmer software package**,
k-mer counting, graph traversal, and sequence processing
github.com/dib-lab/khmer

Member of and contributor to **bioconda channel**,
conda channel for bioinformatics packages for Linux and MacOS
github.com/bioconda/bioconda-recipes

BLOGS AND
SOCIAL MEDIA

GitHub: github.com/camillescott, github.com/camillescottatwork

Blog: camillescott.org

REFERENCES

(Contact details available upon request)